Welcome to the
BioInformatics & Molecular Analysis Section (BIMAS)

HLA Peptide Binding Predictions

Function: Rank potential 8-mer, 9-mer, or 10-mer peptides based on a predicted half-time of dissociation to HLA class I molecules. The analysis is based on coefficient tables deduced from the published literature by Dr. Kenneth Parker kparker@atlas.niaid.nih.gov, NIAID, NIH.
Another web site for predicting which peptides bind to MHC molecules is SYFPEITHI, developed by Hans-Georg Rammensee's lab.

Analysis Options:

HLA molecule

| A1 |
| A_0201 |
| A_0205 |
| A24 |
| A3 |

n-mers

| 9 |

Results Limited by: ● **Explicit Number** ○ **Predicted** $T_{(½)}$ **>=**

| 20 |

| 100 |

Please enter or paste an AA sequence to analyze (most formats accepted):

☑ Echo input sequence (generally recommended)

[submit] [reset]

Credits: WWW implementation by Ronald Taylor of BIMAS / CBEL / CIT / NIH

If you use results from this analysis in published research, please cite:

Parker, K. C., M. A. Bednarek, and J. E. Coligan. 1994. Scheme for ranking potential HLA-A2 binding peptides based on independent binding of individual peptide side-chains. J. Immunol. 152:163.

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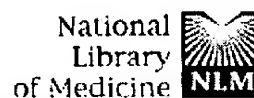
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☐ 1: *AIDS Res Hum Retroviruses* 1997 May 1;13(7):529-31   Books, LinkOut

PubMed Services

Related Resources

An interactive Web site providing major histocompatibility ligand predictions: application to HIV research.

De Groot AS, Jesdale BM, Szu E, Schafer JR, Chicz RM, Deocampo G

TB/HIV Research Laboratory, Brown University School of Medicine, Providence, Rhode Island 02912, USA.

EpiMatrix/HIV, a tool that is currently available on the World Wide Web, enables researchers to screen HIV proteins for potential MHC ligands. We have performed a comparison of EpiMatrix predictions to 158 published allotype-specific HLA-associated peptides (MHC ligands) derived from 133 proteins. The top 10 ranked EpiMatrix predictions for each of the 158 HLA allotype-protein pairs were selected for comparison with these published ligands. EpiMatrix correctly identified 134 of 158 published ligands (85%). The algorithm is now available for use by the HIV research community at the URL http://(/)www.EpiMatrix.com/HIV.

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